2-glycoprotein I); EC 3.4.21.36 (Pancreatic Elastase)

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=> d his

     (FILE 'HOME' ENTERED AT 08:55:04 ON 21 JUL 2004)
               SET COST OFF

     FILE 'HCAPLUS' ENTERED AT 08:55:31 ON 21 JUL 2004
L1             1 S (WO99-EP9440 OR EP98-122969)/AP,PRN
                 E SONDERMANN P/AU
L2            24 S E3,E4
                 E SONDERMAN P/AU
                 E HUBER R/AU
L3          1139 S E3-E14,E40-E48
                 E HUEBER R/AU
L4             6 S E3,E4,E6
                 E HEUBER R/AU
                 E JACOB U/AU
L5            50 S E3,E7
                 E MAX PLANCK/PA,CS
                 E MAXPLANC/PA,CS
L6         92521 S (MAXPLANC? OR MAX()PLANC?)/PA,CS
L7             3 S E45-E49
                 E MAX-PLA/PA,CS
                 E MAXPLA/PA,CS
                 E MAX PLA/PA,CS
L8             3 S E5-E7
                 E MAX PLAU/PA,CS
L9            10 S E5-E14
                 E FC RECEPTOR/CT
                 E E58+ALL
L10           19 S E2
                 E FC RECEPTOR/CT
                 E E31+ALL
L11          202 S E2 (L) (IIB OR IIC)
                 E FC
                 E FCGAMMA
L12            3 S E3(L) (IIB OR IIC)
L13            1 S E10
L14           84 S E26-E29
L15          529 S FC?(L)(IIB OR IIC OR RIIB OR RIIC OR R()(IIB OR IIC))
L16          414 S FC(L)RECEPTOR?(L)(IIB OR IIC OR RIIB OR RIIC OR R()(IIB OR II
L17          358 S L16 (L) GAMMA
L18          398 S L15 (L) ?GAMMA?
L19          358 S L16 (L) ?GAMMA?
L20          452 S L17-L19,L10-L14
L21          121 S L15-L19 NOT L20
L22           46 S L21 AND IMMUNOGLOBULIN
L23          397 S L20 AND IMMUNOGLOBULIN
L24           55 S L20 NOT L23
L25          498 S L20,L22-L24
L26           75 S L10-L24 NOT L25
L27           37 S L25 AND RECOMBIN?
L28           38 S L25 AND CHIMER?
L29           67 S L27,L28
                 E RECOMBINANT/CT
                 E E47+ALL
L30        42218 S E1+NT
                 E E7+ALL
L31        16654 S E3,E4,E2+NT
L32           26 S L25 AND L30,L31
                 E IMMUNOGLOGULIN/CT
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                E IMMUNOGLOBULIN/CT
                E E35+ALL
L33         72507 S E9+OLD,NT,PFT,RT
L34            56 S L33 AND L29,L32
L35            12 S L29,L32 NOT L34
                  SEL DN AN 6
L36             1 S L35 AND E1-E3
L37             8 S L34 NOT ?GAMMA?
L38             7 S L37 AND TYPE()(II OR IIB OR IIC OR IIA)
L39             6 S L37 AND TYPE()(IIB OR IIC)
L40             6 S L37 AND IGG()TYPE()(IIB OR IIC)
L41             5 S L40 NOT MHC/TI
L42             3 S L37 NOT L41
L43            57 S L34,L36,L41
L44            11 S L2-L9 AND L25
L45             3 S L44 AND (RECOMB? OR CHIMER?)
L46             3 S L1,L45
L47             8 S L44 NOT L46
L48             7 S L47 NOT SHIP
L49            10 S L46,L48
L50            19 S L43 AND (PY<=1998 OR PRY<=1998 OR AY<=1998)
L51            27 S L49,L50
L52            27 S L51 AND (IIB OR IIC OR ?RIIB OR ?RIIC OR FC? OR ?GAMMA? OR IM

     FILE 'HCAPLUS' ENTERED AT 09:30:47 ON 21 JUL 2004
                SEL RN L1

     FILE 'REGISTRY' ENTERED AT 09:31:09 ON 21 JUL 2004
L53            21 S E4-E24
L54            12 S L53 AND PROTEIN/FS
L55             1 S L54 AND 185/SQL

     FILE 'HCAPLUS' ENTERED AT 09:31:43 ON 21 JUL 2004
L56             1 S L55

     FILE 'REGISTRY' ENTERED AT 09:31:55 ON 21 JUL 2004

     FILE 'HCAPLUS' ENTERED AT 09:33:19 ON 21 JUL 2004
L57          5300 S FC?(L)(III OR RIII OR R III)
L58          1349 S L57(L)?GAMMA?
L59          1054 S FC(L)RECEPTOR?(L)(III OR RIII OR R III)(L)?GAMMA?
L60          1349 S L58,L59
L61           148 S L60 AND (RECOMBINA? OR CHIMER?)
L62            18 S L60 AND L30,L31
L63           149 S L61,L62
L64           132 S L63 AND IMMUNOGLOBULIN
L65            17 S L63 NOT L64
L66           103 S L64 AND (PY<=1998 OR PRY<=1998 OR AY<=1998)
L67            14 S L2-L9 AND L60
L68             2 S L67 AND L63
L69             1 S L68 NOT RECOMBINASE
L70            12 S L67 NOT L68
L71            10 S L70 NOT (ULTRASONIC OR INTERLEUKIN)/TI
L72            34 S L69,L71,L52
L73           103 S L66 AND ?GAMMA?
L74           103 S L73 AND FC?
L75            83 S L74 AND III
L76            94 S L74 AND ?RIII
L77           103 S L75,L76
L78             9 S L74 NOT L76
L79             8 S L78 AND TYPE III
L80           103 S L77,L76
L81            12 S L80 AND P/DT
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                SEL DN AN 1 3 4 8
L82              4 S E25-E36
L83             96 S L80 NOT L52,L72,L82
                SEL DN AN 30 50 51 71 85 93
L84              6 S E37-E54
L85             44 S L52,L72,L82,L84 AND L1-L52,L56-L84
L86             30 S L85 AND (PY<=1998 OR PRY<=1998 OR AY<=1998)
L87             14 S L85 NOT L86
L88             17 S L85 AND L1-L9
L89             17 S L87,L88
L90             27 S L85 NOT L89

     FILE 'HCAPLUS' ENTERED AT 10:06:09 ON 21 JUL 2004

     FILE 'MEDLINE' ENTERED AT 10:06:49 ON 21 JUL 2004
                E FC RECEPTOR/CT
                E E6+ALL
                E E2+ALL
L91           4709 S E27
                E RECOMBINANT/CT
L92            185 S E13+NT AND L91
L93            497 S E77+NT AND L91
L94            497 S L92,L93
L95            331 S L94 AND PY<=1998
L96             86 S L95 AND (?RIIB? OR ?RIII?)
L97             43 S L95 AND (IIB? OR III?)
L98            106 S L96,L97
L99            104 S L98 AND FC?
L100            94 S L99 AND ?GAMMA?
L101            12 S L98 NOT L100
L102            82 S L100/HUM
L103            12 S L100 NOT L102
L104            20 S L91 AND (SONDERMAN? OR HUBER ? OR HEUBER ? OR HUEBER ? OR JAC
L105             5 S L104 AND PY<=1998
L106             8 S L104 AND ?RIIB
L107             5 S L104 AND ?RIII
L108            11 S L106,L107

     FILE 'MEDLINE' ENTERED AT 10:15:16 ON 21 JUL 2004
L109             9 S L108 NOT (JACOB C? OR JACOB A?)/AU

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 14, 2004, 06:36:34 ; Search time 19 Seconds
(without alignments)
502.674 Million cell updates/sec

Title: US-09-856-933-3
Perfect score: 1006
Sequence: 1 MGTPAAPPKAVLKLEPQWIN.....SSKPVTITVQAPSSSPMGII 185

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	930	92.4	170	4	US-09-245-764-6	Sequence 6, Appli
2	921.5	91.6	307	2	US-08-332-562A-83	Sequence 83, Appl
3	921	91.6	170	4	US-09-245-764-5	Sequence 5, Appli
4	885.5	88.0	345	2	US-08-332-562A-132	Sequence 132, App
5	884	87.9	170	4	US-09-245-764-10	Sequence 10, Appl
6	883	87.8	171	4	US-09-245-764-14	Sequence 14, Appl
7	877	87.2	171	4	US-09-245-764-15	Sequence 15, Appl
8	874	86.9	170	4	US-09-245-764-12	Sequence 12, Appl
9	873	86.8	171	4	US-09-245-764-3	Sequence 3, Appli
10	869	86.4	170	4	US-09-245-764-11	Sequence 11, Appl
11	611	60.7	283	2	US-08-332-562A-136	Sequence 136, App
12	611	60.7	330	2	US-08-332-562A-81	Sequence 81, Appl
13	597	59.3	330	2	US-08-332-562A-134	Sequence 134, App
14	577	57.4	261	2	US-08-332-562A-133	Sequence 133, App
15	451	44.8	87	2	US-08-332-562A-90	Sequence 90, Appl
16	447.5	44.5	233	2	US-08-667-939A-7	Sequence 7, Appli
17	447.5	44.5	233	4	US-08-433-123-7	Sequence 7, Appli
18	438.5	43.6	233	2	US-08-667-939A-5	Sequence 5, Appli
19	438.5	43.6	233	4	US-08-433-123-5	Sequence 5, Appli
20	438	43.5	174	4	US-09-245-764-8	Sequence 8, Appli
21	437.5	43.5	233	2	US-08-667-939A-6	Sequence 6, Appli
22	437.5	43.5	233	4	US-08-433-123-6	Sequence 6, Appli
23	434	43.1	254	2	US-08-667-939A-4	Sequence 4, Appli
24	434	43.1	254	4	US-08-433-123-4	Sequence 4, Appli
25	433.5	43.1	233	2	US-08-667-939A-8	Sequence 8, Appli
26	433.5	43.1	233	4	US-08-433-123-8	Sequence 8, Appli
27	433	43.0	254	2	US-08-667-939A-2	Sequence 2, Appli
28	433	43.0	254	4	US-08-433-123-2	Sequence 2, Appli
29	432	42.9	254	2	US-08-667-939A-3	Sequence 3, Appli
30	432	42.9	254	4	US-08-433-123-3	Sequence 3, Appli
31	428	42.5	203	2	US-08-667-939A-20	Sequence 20, Appl
32	428	42.5	203	4	US-08-433-123-20	Sequence 20, Appl
33	428	42.5	215	2	US-08-667-939A-18	Sequence 18, Appl
34	428	42.5	215	4	US-08-433-123-18	Sequence 18, Appl
35	428	42.5	254	2	US-08-667-939A-9	Sequence 9, Appli
36	428	42.5	254	4	US-08-433-123-9	Sequence 9, Appli
37	422	41.9	254	2	US-08-667-939A-1	Sequence 1, Appli
38	422	41.9	254	4	US-08-433-123-1	Sequence 1, Appli
39	412.5	41.0	83	2	US-08-332-562A-91	Sequence 91, Appl
40	394	39.2	261	4	US-09-245-764-7	Sequence 7, Appli
41	352	35.0	199	3	US-08-833-488B-14	Sequence 14, Appl
42	351	34.9	173	3	US-08-833-488B-31	Sequence 31, Appl
43	351	34.9	197	3	US-08-833-488B-28	Sequence 28, Appl
44	351	34.9	229	3	US-08-833-488B-24	Sequence 24, Appl
45	351	34.9	253	3	US-08-833-488B-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-245-764-6
; Sequence 6, Application US/09245764
; Patent No. 6675105
; GENERAL INFORMATION:
; APPLICANT: Hogarth, P. Mark
; APPLICANT: Powell, Maree S.
; APPLICANT: McKenzie, Ian F.C.
; APPLICANT: Maxwell, Kelly F.
; APPLICANT: Garrett, Thomas P.J.
; APPLICANT: Epa, Vidana
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF Fc RECEPTORS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 4102-4
; CURRENT APPLICATION NUMBER: US/09/245,764
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/099,994
; EARLIER FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: 60/073,972
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-764-6

Query Match 92.4%; Score 930; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 3e-87;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 APPKAVLKLEPQWINVLQEDSVTLTCRGTHSPESDSIQWFHNGNLIPTHTQPSYRFKANN 60

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RESULT 2
US-08-332-562A-83
; Sequence 83, Application US/08332562A
; Patent No. 5985599
; GENERAL INFORMATION: